

J Michael Cherry

List of Publications by Year in descending order

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126
papers

70,582
citations

25034

57
h-index

16650

123
g-index

137
all docs

137
docs citations

137
times ranked

89624
citing authors

#	ARTICLE	IF	CITATIONS
1	Gene Ontology: tool for the unification of biology. <i>Nature Genetics</i> , 2000, 25, 25-29.	21.4	34,499
2	The Genome Sequence of <i>Drosophila melanogaster</i> . <i>Science</i> , 2000, 287, 2185-2195.	12.6	5,566
3	The Gene Ontology Resource: 20 years and still GOing strong. <i>Nucleic Acids Research</i> , 2019, 47, D330-D338.	14.5	3,474
4	The Gene Ontology resource: enriching a GOLD mine. <i>Nucleic Acids Research</i> , 2021, 49, D325-D334.	14.5	2,416
5	Annotation of functional variation in personal genomes using RegulomeDB. <i>Genome Research</i> , 2012, 22, 1790-1797.	5.5	2,335
6	Expansion of the Gene Ontology knowledgebase and resources. <i>Nucleic Acids Research</i> , 2017, 45, D331-D338.	14.5	1,838
7	GO::TermFinder--open source software for accessing Gene Ontology information and finding significantly enriched Gene Ontology terms associated with a list of genes. <i>Bioinformatics</i> , 2004, 20, 3710-3715.	4.1	1,782
8	Saccharomyces Genome Database: the genomics resource of budding yeast. <i>Nucleic Acids Research</i> , 2012, 40, D700-D705.	14.5	1,649
9	Comparative Genomics of the Eukaryotes. <i>Science</i> , 2000, 287, 2204-2215.	12.6	1,573
10	The Encyclopedia of DNA elements (ENCODE): data portal update. <i>Nucleic Acids Research</i> , 2018, 46, D794-D801.	14.5	1,559
11	Expanded encyclopaedias of DNA elements in the human and mouse genomes. <i>Nature</i> , 2020, 583, 699-710.	27.8	1,252
12	The Gene Ontology (GO) project in 2006. <i>Nucleic Acids Research</i> , 2006, 34, D322-D326.	14.5	923
13	SGD: Saccharomyces Genome Database. <i>Nucleic Acids Research</i> , 1998, 26, 73-79.	14.5	912
14	Macronuclear Genome Sequence of the Ciliate <i>Tetrahymena thermophila</i> , a Model Eukaryote. <i>PLoS Biology</i> , 2006, 4, e286.	5.6	657
15	ENCODE data at the ENCODE portal. <i>Nucleic Acids Research</i> , 2016, 44, D726-D732.	14.5	500
16	The Stanford Microarray Database. <i>Nucleic Acids Research</i> , 2001, 29, 152-155.	14.5	415
17	Comparison of the Complete Protein Sets of Worm and Yeast: Orthology and Divergence. , 1998, 282, 2022-2028.		404
18	H3K4me3 Breadth Is Linked to Cell Identity and Transcriptional Consistency. <i>Cell</i> , 2014, 158, 673-688.	28.9	404

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19	Evaluating the Clinical Validity of Gene-Disease Associations: An Evidence-Based Framework Developed by the Clinical Genome Resource. <i>American Journal of Human Genetics</i> , 2017, 100, 895-906.	6.2	403
20	<i>Arabidopsis thaliana</i> : A Model Plant for Genome Analysis. , 1998, 282, 662-682.		397
21	New developments on the Encyclopedia of DNA Elements (ENCODE) data portal. <i>Nucleic Acids Research</i> , 2020, 48, D882-D889.	14.5	381
22	SOURCE: a unified genomic resource of functional annotations, ontologies, and gene expression data. <i>Nucleic Acids Research</i> , 2003, 31, 219-223.	14.5	376
23	The Reference Genome Sequence of <i>Saccharomyces cerevisiae</i> : Then and Now. <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 389-398.	1.8	369
24	GENETICS: Yeast as a Model Organism. <i>Science</i> , 1997, 277, 1259-1260.	12.6	362
25	<i>Saccharomyces</i> Genome Database (SGD) provides secondary gene annotation using the Gene Ontology (GO). <i>Nucleic Acids Research</i> , 2002, 30, 69-72.	14.5	322
26	YeastMine—an integrated data warehouse for <i>Saccharomyces cerevisiae</i> data as a multipurpose tool-kit. <i>Database: the Journal of Biological Databases and Curation</i> , 2012, 2012, bar062.	3.0	282
27	<i>Saccharomyces</i> Genome Database (SGD) provides tools to identify and analyze sequences from <i>Saccharomyces cerevisiae</i> and related sequences from other organisms. <i>Nucleic Acids Research</i> , 2004, 32, 311D-314.	14.5	258
28	An atlas of dynamic chromatin landscapes in mouse fetal development. <i>Nature</i> , 2020, 583, 744-751.	27.8	257
29	Gene Ontology annotations at SGD: new data sources and annotation methods. <i>Nucleic Acids Research</i> , 2007, 36, D577-D581.	14.5	218
30	Identification of unstable transcripts in <i>Arabidopsis</i> by cDNA microarray analysis: Rapid decay is associated with a group of touch- and specific clock-controlled genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 11513-11518.	7.1	200
31	<i>Saccharomyces</i> genome database. <i>Methods in Enzymology</i> , 2002, 350, 329-346.	1.0	188
32	A gene ontology inferred from molecular networks. <i>Nature Biotechnology</i> , 2013, 31, 38-45.	17.5	184
33	RNAcentral: a comprehensive database of non-coding RNA sequences. <i>Nucleic Acids Research</i> , 2017, 45, D128-D134.	14.5	174
34	PatMatch: a program for finding patterns in peptide and nucleotide sequences. <i>Nucleic Acids Research</i> , 2005, 33, W262-W266.	14.5	162
35	RNAcentral: a hub of information for non-coding RNA sequences. <i>Nucleic Acids Research</i> , 2019, 47, D221-D229.	14.5	153
36	The Gene Ontology's Reference Genome Project: A Unified Framework for Functional Annotation across Species. <i>PLoS Computational Biology</i> , 2009, 5, e1000431.	3.2	148

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37	Genetic and physical maps of <i>Saccharomyces cerevisiae</i> . <i>Nature</i> , 1997, 387, 67-73.	27.8	145
38	Alliance of Genome Resources Portal: unified model organism research platform. <i>Nucleic Acids Research</i> , 2020, 48, D650-D658.	14.5	145
39	A guide to best practices for Gene Ontology (GO) manual annotation. <i>Database: the Journal of Biological Databases and Curation</i> , 2013, 2013, bat054-bat054.	3.0	135
40	An integrated genetic/RFLP map of the <i>Arabidopsis thaliana</i> genome. <i>Plant Journal</i> , 1993, 3, 745-754.	5.7	123
41	Perspectives on ENCODE. <i>Nature</i> , 2020, 583, 693-698.	27.8	123
42	The internally located telomeric sequences in the germ-line chromosomes of <i>tetrahymena</i> are at the ends of transposon-like elements. <i>Cell</i> , 1985, 43, 747-758.	28.9	110
43	<i>Saccharomyces</i> Genome Database provides mutant phenotype data. <i>Nucleic Acids Research</i> , 2010, 38, D433-D436.	14.5	108
44	<i>Tetrahymena</i> Genome Database (TGD): a new genomic resource for <i>Tetrahymena thermophila</i> research. <i>Nucleic Acids Research</i> , 2006, 34, D500-D503.	14.5	107
45	RNAcentral: an international database of ncRNA sequences. <i>Nucleic Acids Research</i> , 2015, 43, D123-D129.	14.5	103
46	<i>Saccharomyces cerevisiae</i> S288C genome annotation: a working hypothesis. <i>Yeast</i> , 2006, 23, 857-865.	1.7	99
47	Inference of combinatorial regulation in yeast transcriptional networks: A case study of sporulation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 1998-2003.	7.1	95
48	GA4GH: International policies and standards for data sharing across genomic research and healthcare. <i>Cell Genomics</i> , 2021, 1, 100029.	6.5	94
49	Integrating functional genomic information into the <i>Saccharomyces</i> Genome Database. <i>Nucleic Acids Research</i> , 2000, 28, 77-80.	14.5	93
50	Genome Snapshot: a new resource at the <i>Saccharomyces</i> Genome Database (SGD) presenting an overview of the <i>Saccharomyces cerevisiae</i> genome. <i>Nucleic Acids Research</i> , 2006, 34, D442-D445.	14.5	91
51	A systematic approach to reconstructing transcription networks in <i>Saccharomyces cerevisiae</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 16893-16898.	7.1	84
52	<i>Saccharomyces</i> genome database: Underlying principles and organisation. <i>Briefings in Bioinformatics</i> , 2004, 5, 9-22.	6.5	83
53	Combining guilt-by-association and guilt-by-profiling to predict <i>Saccharomyces cerevisiae</i> gene function. <i>Genome Biology</i> , 2008, 9, S7.	9.6	78
54	Microarray data quality analysis: lessons from the AFGC project. <i>Arabidopsis Functional Genomics Consortium</i> . <i>Plant Molecular Biology</i> , 2002, 48, 119-132.	3.9	76

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55	Mutational analysis of conserved nucleotides in a self-splicing group I intron. <i>Journal of Molecular Biology</i> , 1990, 215, 345-358.	4.2	73
56	AGAPE (Automated Genome Analysis PipelinE) for Pan-Genome Analysis of <i>Saccharomyces cerevisiae</i> . <i>PLoS ONE</i> , 2015, 10, e0120671.	2.5	73
57	Expanded protein information at SGD: new pages and proteome browser. <i>Nucleic Acids Research</i> , 2007, 35, D468-D471.	14.5	69
58	Using the <i>Saccharomyces</i> Genome Database (SGD) for analysis of protein similarities and structure. <i>Nucleic Acids Research</i> , 1999, 27, 74-78.	14.5	66
59	<i>Saccharomyces</i> Genome Database provides tools to survey gene expression and functional analysis data. <i>Nucleic Acids Research</i> , 2001, 29, 80-81.	14.5	61
60	A short study on the success of the Gene Ontology. <i>Web Semantics</i> , 2004, 1, 235-240.	2.9	61
61	<i>Saccharomyces</i> genome database provides new regulation data. <i>Nucleic Acids Research</i> , 2014, 42, D717-D725.	14.5	59
62	<i>Saccharomyces</i> Genome Database (SGD) provides biochemical and structural information for budding yeast proteins. <i>Nucleic Acids Research</i> , 2003, 31, 216-218.	14.5	57
63	Harmonizing model organism data in the Alliance of Genome Resources. <i>Genetics</i> , 2022, 220, .	2.9	52
64	Functional annotations for the <i>Saccharomyces cerevisiae</i> genome: the knowns and the known unknowns. <i>Trends in Microbiology</i> , 2009, 17, 286-294.	7.7	49
65	Appendix D: Codon Usage Table for <i>Xenopus laevis</i> . <i>Methods in Cell Biology</i> , 1991, 36, 675-677.	1.1	46
66	Fungal BLAST and Model Organism BLASTP Best Hits: new comparison resources at the <i>Saccharomyces</i> Genome Database (SGD). <i>Nucleic Acids Research</i> , 2004, 33, D374-D377.	14.5	46
67	Ontology application and use at the ENCODE DCC. <i>Database: the Journal of Biological Databases and Curation</i> , 2015, 2015, .	3.0	42
68	The new modern era of yeast genomics: community sequencing and the resulting annotation of multiple <i>Saccharomyces cerevisiae</i> strains at the <i>Saccharomyces</i> Genome Database. <i>Database: the Journal of Biological Databases and Curation</i> , 2013, 2013, bat012.	3.0	40
69	Principles of metadata organization at the ENCODE data coordination center. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, baw001.	3.0	40
70	ClinGen Variant Curation Interface: a variant classification platform for the application of evidence criteria from ACMG/AMP guidelines. <i>Genome Medicine</i> , 2022, 14, 6.	8.2	34
71	New data and collaborations at the <i>Saccharomyces</i> Genome Database: updated reference genome, alleles, and the Alliance of Genome Resources. <i>Genetics</i> , 2022, 220, .	2.9	34
72	Towards BioDBcore: a community-defined information specification for biological databases. <i>Nucleic Acids Research</i> , 2011, 39, D7-D10.	14.5	32

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73	Molecular linguistics: Extracting information from gene and protein sequences. Proceedings of the National Academy of Sciences of the United States of America, 1997, 94, 5506-5507.	7.1	31
74	Active Interaction Mapping Reveals the Hierarchical Organization of Autophagy. Molecular Cell, 2017, 65, 761-774.e5.	9.7	31
75	Towards BioDBcore: a community-defined information specification for biological databases. Database: the Journal of Biological Databases and Curation, 2011, 2011, baq027-baq027.	3.0	30
76	AtDB, the Arabidopsis thaliana database, and graphical-web-display of progress by the Arabidopsis Genome Initiative. Nucleic Acids Research, 1998, 26, 80-84.	14.5	29
77	Data Sanitization to Reduce Private Information Leakage from Functional Genomics. Cell, 2020, 183, 905-917.e16.	28.9	28
78	Saccharomyces genome database informs human biology. Nucleic Acids Research, 2018, 46, D736-D742.	14.5	27
79	InterMOD: integrated data and tools for the unification of model organism research. Scientific Reports, 2013, 3, 1802.	3.3	25
80	The <i>Saccharomyces</i> Genome Database: A Tool for Discovery. Cold Spring Harbor Protocols, 2015, 2015, pdb.top083840.	0.3	24
81	New mutant phenotype data curation system in the Saccharomyces Genome Database. Database: the Journal of Biological Databases and Curation, 2009, 2009, bap001-bap001.	3.0	23
82	TheSaccharomycesGenome Database Variant Viewer. Nucleic Acids Research, 2016, 44, D698-D702.	14.5	23
83	The ENCODE Portal as an Epigenomics Resource. Current Protocols in Bioinformatics, 2019, 68, e89.	25.8	23
84	AAAtDB, anArabidopsis thaliana database. Plant Molecular Biology Reporter, 1992, 10, 308-309.	1.8	20
85	Genome comparisons highlight similarity and diversity within the eukaryotic kingdoms. Current Opinion in Chemical Biology, 2001, 5, 86-89.	6.1	19
86	Genetic Dissection of an RNA Enzyme. Cold Spring Harbor Symposia on Quantitative Biology, 1987, 52, 173-180.	1.1	18
87	Curated protein information in the Saccharomyces genome database. Database: the Journal of Biological Databases and Curation, 2017, 2017, .	3.0	17
88	Using computational predictions to improve literature-based Gene Ontology annotations: a feasibility study. Database: the Journal of Biological Databases and Curation, 2011, 2011, bar004-bar004.	3.0	16
89	Unified display of Arabidopsis thaliana physical maps from AtDB, the A.thaliana database. Nucleic Acids Research, 1999, 27, 79-84.	14.5	15
90	Integration of new alternative reference strain genome sequences into theSaccharomycesgenome database. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw074.	3.0	15

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91	Providing Access to Genomic Variant Knowledge in a Healthcare Setting: A Vision for the ClinGen Electronic Health Records Workgroup. <i>Clinical Pharmacology and Therapeutics</i> , 2016, 99, 157-160.	4.7	15
92	Transcriptome visualization and data availability at the <i>Saccharomyces</i> Genome Database. <i>Nucleic Acids Research</i> , 2020, 48, D743-D748.	14.5	15
93	In the beginning there was babble. <i>Autophagy</i> , 2012, 8, 1165-1167.	9.1	14
94	CNN-Peaks: ChIP-Seq peak detection pipeline using convolutional neural networks that imitate human visual inspection. <i>Scientific Reports</i> , 2020, 10, 7933.	3.3	14
95	SnoVault and encodedD: A novel object-based storage system and applications to ENCODE metadata. <i>PLoS ONE</i> , 2017, 12, e0175310.	2.5	14
96	Toward an interactive article: integrating journals and biological databases. <i>BMC Bioinformatics</i> , 2011, 12, 175.	2.6	12
97	Expanding yeast knowledge online. , 1998, 14, 1453-1469.		11
98	Mining experimental evidence of molecular function claims from the literature. <i>Bioinformatics</i> , 2007, 23, 3232-3240.	4.1	11
99	The YeastGenome app: the <i>Saccharomyces</i> Genome Database at your fingertips. <i>Database: the Journal of Biological Databases and Curation</i> , 2013, 2013, bat004.	3.0	11
100	<i>Saccharomyces cerevisiae</i> homoserine kinase is homologous to prokaryotic homoserine kinases. <i>Gene</i> , 1990, 96, 177-180.	2.2	10
101	Considerations for creating and annotating the budding yeast Genome Map at SGD: a progress report. <i>Database: the Journal of Biological Databases and Curation</i> , 2012, 2012, bar057-bar057.	3.0	10
102	The <i>Saccharomyces</i> Genome Database: Advanced Searching Methods and Data Mining. <i>Cold Spring Harbor Protocols</i> , 2015, 2015, pdb.prot088906.	0.3	10
103	CvManGO, a method for leveraging computational predictions to improve literature-based Gene Ontology annotations. <i>Database: the Journal of Biological Databases and Curation</i> , 2012, 2012, bas001.	3.0	9
104	From one to many: expanding the <i>Saccharomyces cerevisiae</i> reference genome panel. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, baw020.	3.0	9
105	Prevention of data duplication for high throughput sequencing repositories. <i>Database: the Journal of Biological Databases and Curation</i> , 2018, 2018, .	3.0	9
106	Characteristics of Amino Acids. <i>Current Protocols in Molecular Biology</i> , 1996, 33, Appendix 1C.	2.9	7
107	Integration of macromolecular complex data into the <i>Saccharomyces</i> Genome Database. <i>Database: the Journal of Biological Databases and Curation</i> , 2019, 2019, .	3.0	7
108	Objective: The Complete Sequence of a Plant Genome. <i>Plant Cell</i> , 1997, 9, 476.	6.6	6

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109	TheSaccharomycesGenome Database: Gene Product Annotation of Function, Process, and Component. Cold Spring Harbor Protocols, 2015, 2015, pdb.prot088914.	0.3	6
110	XenMine: A genomic interaction tool for the Xenopus community. Developmental Biology, 2017, 426, 155-164.	2.0	6
111	Outreach and online training services at the Saccharomyces Genome Database. Database: the Journal of Biological Databases and Curation, 2017, 2017, .	3.0	6
112	TheSaccharomycesGenome Database: Exploring Biochemical Pathways and Mutant Phenotypes. Cold Spring Harbor Protocols, 2015, 2015, pdb.prot088898.	0.3	5
113	ACEDB: A Tool for Biological Information. , 1994, , 347-356.		4
114	Integrative Meta-Assembly Pipeline (IMAP): Chromosome-level genome assembler combining multiple de novo assemblies. PLoS ONE, 2019, 14, e0221858.	2.5	3
115	A Short Study on the Success of the Gene Ontology. SSRN Electronic Journal, 0, , .	0.4	3
116	Computer Manipulation of DNA and Protein Sequences. Current Protocols in Molecular Biology, 1995, 30, Unit7.7.	2.9	2
117	The arabidopsis database moves to Stanford. Plant Molecular Biology Reporter, 1996, 14, 6-8.	1.8	2
118	The <i>Saccharomyces</i> Genome Database: Exploring Genome Features and Their Annotations. Cold Spring Harbor Protocols, 2015, 2015, pdb.prot088922.	0.3	2
119	Updated regulation curation model at the Saccharomyces Genome Database. Database: the Journal of Biological Databases and Curation, 2018, 2018, .	3.0	2
120	Incorporation of a unified protein abundance dataset into the Saccharomyces genome database. Database: the Journal of Biological Databases and Curation, 2020, 2020, .	3.0	2
121	Microarray data quality analysis: lessons from the AFGC project. , 2002, , 119-131.		2
122	An integrated genetic/RFLP map of the Arabidopsis thaliana genome. Plant Journal, 1993, 3, 745-754.	5.7	2
123	Gene function, metabolic pathways and comparative genomics in yeast. , 0, , .		1
124	DATABASE, The Journal of Biological Databases and Curation, is now the official journal of the International Society for Biocuration. Database: the Journal of Biological Databases and Curation, 2013, 2013, bat077-bat077.	3.0	1
125	An integrated RFLP map of Arabidopsis thaliana. Advances in Cellular and Molecular Biology of Plants, 1994, , 159-162.	0.2	1
126	Computational Methods and Bioinformatic Tools. , 0, , 769-904.		0